

## CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/430,590ECRF Processing Date: \_\_\_\_\_  
Edited by: \_\_\_\_\_  
Verified by: \_\_\_\_\_ (STIC staff)

#20

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: Authorized edit. Inserted <220> to <223> information  
for sequence # 150

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

1636

## RAW SEQUENCE LISTING

DATE: 05/09/2001

PATENT APPLICATION: US/09/430,590E

TIME: 12:13:03

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\05092001\I430590E.raw

3 <110> APPLICANT: Poulter, et al.  
5 <120> TITLE OF INVENTION: UNUSUAL RETROTRANSPOSON FROM THE YEAST CANDIDA ALBICANS  
7 <130> FILE REFERENCE: 674521-2001.1  
9 <140> CURRENT APPLICATION NUMBER: 09/430,590E  
10 <141> CURRENT FILING DATE: 1999-10-29  
12 <150> PRIOR APPLICATION NUMBER: 60/106,342  
13 <151> PRIOR FILING DATE: 1998-10-30  
15 <160> NUMBER OF SEQ ID NOS: 156  
17 <170> SOFTWARE: PatentIn version 3.0  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 388  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Candida albicans  
24 <300> PUBLICATION INFORMATION:  
25 <308> DATABASE ACCESSION NO: AF043301  
26 <309> DATABASE ENTRY DATE: 1998-07-21  
27 <313> RELEVANT RESIDUES: (1)..(388)  
29 <400> SEQUENCE: 1

30	tgttcgctat agagagat	ttt cctagccgga atgcacgaca atcctgagac ggaagtcgat	60
32	cgtcgatgcc catggtgcgt	ggtgaaaaat ttcttagaa aatttggtct ttccttcaac	120
34	tgcttttaag aaagagaggt	tcaagtgggt taagtacgac ggtcacaaag attgcggctt	180
36	atgaggcccg aactgagttg	aaatacaaaa tcaagatata attatatacc ttacttgtcc	240
38	atattgtttt ataatacatt	cttcagatat ttaaatttct gtgtatcaac ctataaaaca	300
40	gagatacatt cagtgcattt	agtatactga gtgaactggt acctgtgaca ttcaagataa	360
42	ctgtttcgcg cacgctggca	gacgaaca	388

45 <210> SEQ ID NO: 2  
46 <211> LENGTH: 400  
47 <212> TYPE: DNA  
48 <213> ORGANISM: Candida albicans  
50 <300> PUBLICATION INFORMATION:  
51 <308> DATABASE ACCESSION NO: Y08494  
52 <309> DATABASE ENTRY DATE: 1997-08-27  
53 <313> RELEVANT RESIDUES: (1)..(400)  
55 <400> SEQUENCE: 2

56	cgggttaatg tatatttcga	cttgcaggac ctatagaaca gctgtagatg taaacactaa	60
58	tatgaagaac tgggaaaaca	ataacttcta ttctgactct gattctgtat gaaaactaac	120
60	tgaagaaaag aatataaaaa	tataaaatat ataagaagac aaaggagaat ctctgaccct	180
62	tatatagacc gaaaactaga	gtgacgatga accatcagac cagtcaataa ccaactaatt	240
64	taataatatc aataactcgt	ctaacgaggt gtaaacaana taccgaaaat agaaatataa	300
66	ataactcaat gccaagatgg	tgcgcaacca ccaaggtaat aaacaacca tagaaccaag	360
68	aattgtaaat cagacaacga	gcaaggctga ttatacaaca	400

71 <210> SEQ ID NO: 3  
72 <211> LENGTH: 6426  
73 <212> TYPE: DNA  
74 <213> ORGANISM: Candida albicans  
76 <220> FEATURE:  
77 <221> NAME/KEY: CDS

see p. 5

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Input Set : A:\Cpg.pto

Output Set: N:\CRF3\05092001\I430590E.raw

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78 <222> LOCATION: (398)..(1372)
79 <223> OTHER INFORMATION: ORF1 coding sequence for gag
82 <220> FEATURE:
83 <221> NAME/KEY: CDS
84 <222> LOCATION: (1373)..(6103)
85 <223> OTHER INFORMATION: ORF2 - coding sequence for pol
88 <400> SEQUENCE: 3
89 tgttggtttg tgcactat ttt tgtgtcagaa actgatcaat gaaaatgatg gttattatga      60
91 gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt      120
93 ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt      180
95 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt      240
97 acacgctcaa tctcaggtaa agaaagttta tattccatca gattagaagt cgatagtgat      300
99 aatcatttcg tcccaaatta gcgttgatata aattcagtc ttagatttgt attattgatt      360
101 gatagtttcg aagtttgaag gtacagaatt tcacaag atg agt tcc gca aag aat      415
102                                     Met Ser Ser Ala Lys Asn
103                                     1           5
105 gat gat aac gaa ggg aag gtc atg gaa agt gtt gat caa gct aat gct      463
106 Asp Asp Asn Glu Gly Lys Val Met Glu Ser Val Asp Gln Ala Asn Ala
107                                     10           20
109 att agt aag gtg gat gaa cat atc aag gct aga ttc aat atg ctt ttc      511
110 Ile Ser Lys Val Asp Glu His Ile Lys Ala Arg Phe Asn Met Leu Phe
111                                     25           30           35
113 ata aaa ttt aat gac tta cct aag ttg gcc gtc ggt aat cag aaa agc      559
114 Ile Lys Phe Asn Asp Leu Pro Lys Leu Ala Val Gly Asn Gln Lys Ser
115                                     40           45           50
117 gtg gat aaa tgg aat gaa gaa ttt aaa tat ttc cac gtt gct tac ccc      607
118 Val Asp Lys Trp Asn Glu Glu Phe Lys Tyr Phe His Val Ala Tyr Pro
119 55                                     60           65           70
121 gat gtt ttg gaa ttt ttg ctt gac tat aat cct aaa gat aaa ttc aag      655
122 Asp Val Leu Glu Phe Leu Leu Asp Tyr Asn Pro Lys Asp Lys Phe Lys
123                                     75           80           85
125 gtt aaa aag gta gaa ggt att tat ttt act ggt tgg tgt tta caa atg      703
126 Val Lys Lys Val Glu Gly Ile Tyr Phe Thr Gly Trp Cys Leu Gln Met
127                                     90           95           100
129 tgt tta cag tcc att ttt gat agg ttc aga ttg atc atg att tct aag      751
130 Cys Leu Gln Ser Ile Phe Asp Arg Phe Arg Leu Ile Met Ile Ser Lys
131                                     105          110          115
133 cta cca aag cac ttg caa aag gaa gca aac tta atc aaa gct gct tat      799
134 Leu Pro Lys His Leu Gln Lys Glu Ala Asn Leu Ile Lys Ala Ala Tyr
135                                     120          125          130
137 gat gct gtt act aaa tct aaa gat tat acc att act agt aag atc ttg      847
138 Asp Ala Val Thr Lys Ser Lys Asp Tyr Thr Ile Thr Ser Lys Ile Leu
139 135                                     140          145          150
141 ctg aag ttt gta aac gtt gaa cat gag tta gtg gtt tgc tat aac ctt      895
142 Ser Lys Phe Val Asn Val Glu His Glu Leu Val Val Cys Tyr Asn Leu
143                                     155          160          165
145 cca tat ttg ctg cag gtg gaa gag aaa ctt gag gaa ata ctc tac aac      943
146 Pro Tyr Leu Ser Gln Val Glu Glu Lys Leu Glu Glu Ile Leu Tyr Asn
147                                     170          175          180

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149	act	tca	aac	ggt	gtc	gat	gag	tat	gtc	cgt	agt	ctt	cca	aat	ctc	ata	991
150	Thr	Ser	Asn	Val	Val	Asp	Glu	Tyr	Val	Arg	Ser	Leu	Pro	Asn	Leu	Ile	
151			185					190					195				
153	ggt	caa	gtc	ttg	tac	ttc	aat	cat	gtg	aag	aaa	tca	gag	gct	tta	agt	1039
154	Gly	Gln	Val	Leu	Tyr	Phe	Asn	His	Val	Lys	Lys	Ser	Glu	Ala	Leu	Ser	
155		200					205					210					
157	ttg	ttt	ttg	aat	att	cat	gcc	tca	tac	tac	tca	aag	tgg	att	caa	gct	1087
158	Leu	Phe	Leu	Asn	Ile	His	Ala	Ser	Tyr	Tyr	Ser	Lys	Trp	Ile	Gln	Ala	
159	215					220					225				230		
161	gac	aat	gat	aca	tca	gta	ctc	cca	agt	tgc	tct	acc	ata	gct	gaa	gaa	1135
162	Asp	Asn	Asp	Thr	Ser	Val	Leu	Pro	Ser	Cys	Ser	Thr	Ile	Ala	Glu	Glu	
163				235						240				245			
165	atg	tgt	gat	cat	cct	gat	tat	gct	aga	ttg	ggt	gac	att	cca	agc	aac	1183
166	Met	Cys	Asp	His	Pro	Asp	Tyr	Ala	Arg	Leu	Val	Asp	Ile	Pro	Ser	Asn	
167			250					255				260					
169	aaa	tat	gaa	ctt	aat	ctt	att	ggt	agt	tta	cca	gca	cca	gag	aaa	cca	1231
170	Lys	Tyr	Glu	Leu	Asn	Leu	Ile	Val	Ser	Leu	Pro	Ala	Pro	Glu	Lys	Pro	
171			265				270					275					
173	aaa	gga	aaa	cca	gag	gag	aac	tca	ctg	gaa	caa	tct	caa	aag	aag	aac	1279
174	Lys	Gly	Lys	Pro	Glu	Glu	Asn	Ser	Ser	Glu	Gln	Ser	Gln	Lys	Lys	Asn	
175		280					285					290					
177	ctg	aaa	tca	aga	aag	aga	aat	aag	aaa	cat	cca	aaa	tca	gat	aac	gat	1327
178	Ser	Lys	Ser	Arg	Lys	Arg	Asn	Lys	Lys	His	Pro	Lys	Ser	Asp	Asn	Asp	
179	295					300				305				310			
181	aaa	ggt	gaa	aaa	gaa	aaa	gaa	aaa	gaa	aaa	act	tca	ctg	gaa	tga	aaa	1375
182	Lys	Gly	Glu	Lys	Glu	Lys	Glu	Lys	Glu	Lys	Thr	Ser	Ser	Glu		Lys	
183				315						320				325			
185	aca	ggt	gct	gct	tct	att	aat	tgt	gta	atg	aat	ata	cat	aat	tgc	agc	1423
186	Thr	Gly	Ala	Ala	Ser	Ile	Asn	Cys	Val	Met	Asn	Ile	His	Asn	Cys	Ser	
187				330						335				340			
189	aaa	acc	acg	ttt	cca	gta	gaa	aat	tct	cat	tct	ctt	aat	gct	tct	ttg	1471
190	Lys	Thr	Thr	Phe	Pro	Val	Glu	Asn	Ser	His	Ser	Leu	Asn	Ala	Ser	Leu	
191				345						350				355			
193	aac	gta	atg	aat	ttt	aaa	ggt	tta	agg	ttt	aac	aag	tat	cta	gtg	tat	1519
194	Asn	Val	Met	Asn	Phe	Lys	Gly	Leu	Arg	Phe	Asn	Lys	Tyr	Leu	Val	Tyr	
195			360					365				370					
197	gat	act	ggt	gcc	aca	ata	tct	ggt	gtg	aac	aat	aaa	gat	ata	ttg	ctg	1567
198	Asp	Thr	Gly	Ala	Thr	Ile	Ser	Val	Val	Asn	Asn	Lys	Asp	Ile	Leu	Ser	
199		375					380					385					
201	aat	ggt	aag	gac	gca	aca	att	gaa	ggt	tct	ggt	gct	gat	ggt	gct	aca	1615
202	Asn	Val	Lys	Asp	Ala	Thr	Ile	Glu	Val	Ser	Val	Ala	Asp	Gly	Ala	Thr	
203	390					395					400				405		
205	tta	gaa	gca	gat	tgt	att	ggt	gat	cta	att	atc	aga	gtc	ggt	att	gtc	1663
206	Leu	Glu	Ala	Asp	Cys	Ile	Gly	Asp	Leu	Ile	Ile	Arg	Val	Gly	Ile	Val	
207				410						415				420			
209	tcg	att	acg	tta	gag	aat	aca	ttg	tat	tta	cca	gaa	agt	tcc	ttt	aat	1711
210	Ser	Ile	Thr	Leu	Glu	Asn	Thr	Leu	Tyr	Leu	Pro	Glu	Ser	Ser	Phe	Asn	
211				425						430				435			
213	ctt	gtg	agt	ttg	aaa	caa	att	gaa	gaa	cga	gga	ttt	aat	ggt	ctt	att	1759

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214 Leu Val Ser Leu Lys Gln Ile Glu Glu Arg Gly Phe Asn Val Leu Ile
215          440          445          450
217 act aaa gaa tca gtg att gta ttt aac caa aat gtg gct cct act att      1807
218 Thr Lys Glu Ser Val Ile Val Phe Asn Gln Asn Val Ala Pro Thr Ile
219          455          460          465
221 att gct tca agg aag aat gct gct gat ctt tat atg ggt cct caa ttc      1855
222 Ile Ala Ser Arg Lys Asn Ala Ala Asp Leu Tyr Met Gly Pro Gln Phe
223 470          475          480          485
225 agt gaa gaa tct tta gaa tgt gat ttt gat tat gat ggt ttg gca gat      1903
226 Ser Glu Glu Ser Leu Glu Cys Asp Phe Asp Tyr Asp Gly Leu Ala Asp
227          490          495          500
229 atg ttg tcc aat gct aac caa gat gac aaa gat aaa tca agt atg aat      1951
230 Met Leu Ser Asn Ala Asn Gln Asp Asp Lys Asp Lys Ser Ser Met Asn
231          505          510          515
233 gaa atg tca gaa tat caa gaa cat gat tat agt tct cga gca tta ata      1999
234 Glu Met Ser Glu Tyr Gln Glu His Asp Tyr Ser Ser Arg Ala Leu Ile
235          520          525          530
237 aat tct ttg acg gag gtt gat gtt tta gat gtt gaa att tcc cca tat      2047
238 Asn Ser Leu Thr Glu Val Asp Val Leu Asp Val Glu Ile Ser Pro Tyr
239          535          540          545
241 gga gtt gaa caa ttg cta cca act gga gat aag aac gat att tat aat      2095
242 Gly Val Glu Gln Leu Leu Pro Thr Gly Asp Lys Asn Asp Ile Tyr Asn
243 550          555          560          565
245 ttc cat ttg atg tca aat cat atg tcc att gag aaa atc ttg ttg tta      2143
246 Phe His Leu Met Ser Asn His Met Ser Ile Glu Lys Ile Leu Leu Leu
247          570          575          580
249 caa aaa tac cag ggt ctc gta ctt cac act tca aaa gag agt ctt caa      2191
250 Gln Lys Tyr Gln Gly Leu Val Leu His Thr Ser Lys Glu Ser Leu Gln
251          585          590          595
253 aag att gct gat tgt aag gta tgt cta tta tcg aat gcc aaa cag aga      2239
254 Lys Ile Ala Asp Cys Lys Val Cys Leu Leu Ser Asn Ala Lys Gln Arg
255          600          605          610
257 agt cac aat cat cat tca gaa aga aaa gcc tcg aga aga cat gag aga      2287
258 Ser His Asn His His Ser Glu Arg Lys Ala Ser Arg Arg His Glu Arg
259          615          620          625
261 ctt cat tgt gat act ctc ggt cca ttt agg tcc gaa aat aac aag tgg      2335
262 Leu His Cys Asp Thr Leu Gly Pro Phe Arg Ser Glu Asn Asn Lys Trp
263 630          635          640          645
265 tat tta acg tct gtt ata gat gaa cat acg ggt tac att gaa gga att      2383
266 Tyr Leu Thr Ser Val Ile Asp Glu His Thr Gly Tyr Ile Glu Gly Ile
267          650          655          660
269 att act aaa gac aga aag gta aag gat ctc tta att caa cga tta aag      2431
270 Ile Thr Lys Asp Arg Lys Val Lys Asp Leu Leu Ile Gln Arg Leu Lys
271          665          670          675
273 atc tgg aat aat cgg ttt aac gat aag gtg gca tac ttc aga agt gat      2479
274 Ile Trp Asn Asn Arg Phe Asn Asp Lys Val Ala Tyr Phe Arg Ser Asp
275          680          685          690
277 aat gct cct gag ttc cca caa cct tct gat tta gct gag ttc ggt att      2527
278 Asn Ala Pro Glu Phe Pro Gln Pro Ser Asp Leu Ala Glu Phe Gly Ile

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Input Set : A:\Cpg.pto

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279      695      700      705
281 tgg agg gag act ata gcg gca tat ctg cct gag ctt aat ggt ctc gcc      2575
282 Trp Arg Glu Thr Ile Ala Ala Tyr Ser Pro Glu Leu Asn Gly Leu Ala
283 710      715      720      725
285 gag gtt gtt aat aaa ttg att tta caa cag att tac agg atc gtt gtg      2623
286 Glu Val Val Asn Lys Leu Ile Leu Gln Gln Ile Tyr Arg Ile Val Val
287      730      735      740
289 aca ctt ggt cca caa ata ctc aag ttg att tat tat gtg att caa tat      2671
290 Thr Leu Gly Pro Gln Ile Leu Lys Leu Ile Tyr Tyr Val Ile Gln Tyr
291      745      750      755
293 tct att aca atg atc aac cac act cca cgt cgt tca ctc aag gga caa      2719
294 Ser Ile Thr Met Ile Asn His Thr Pro Arg Arg Ser Leu Lys Gly Gln
295      760      765      770
297 acc cct tat ggt tgc tat tat caa tta agt gag gga aat ttc tac cgg      2767
298 Thr Pro Tyr Gly Cys Tyr Tyr Gln Leu Ser Glu Gly Asn Phe Tyr Arg
299      775      780      785
301 ttt cct ttt gcc atc gat tgt gtc gtt aca ttt agt aat gcc atc gaa      2815
302 Phe Pro Phe Ala Ile Asp Cys Val Val Thr Phe Ser Asn Ala Ile Glu
303 790      795      800      805
305 aag aac cgt tac gga gtt aca tca act aaa gga gct cct tca tcg atc      2863
306 Lys Asn Arg Tyr Gly Val Thr Ser Thr Lys Gly Ala Pro Ser Ser Ile
307      810      815      820
309 atg ggt gct gtg att ggc tac gct agc gat tgt ttt agt tat tac gtg      2911
310 Met Gly Ala Val Ile Gly Tyr Ala Ser Asp Cys Phe Ser Tyr Tyr Val
311      825      830      835
313 ttg cta aaa aat atg cgg tgt gat att atc ctt agc cct aat gtc cgt      2959
314 Leu Leu Lys Asn Met Arg Cys Asp Ile Ile Leu Ser Pro Asn Val Arg
315      840      845      850
317 ata ttg cga agc tat gag gtt att aac tcc tat ctc aaa aac tta tcc      3007
318 Ile Leu Arg Ser Tyr Glu Val Ile Asn Ser Tyr Leu Lys Asn Leu Ser
319      855      860      865
321 act aca cct atg tca cac att gtt cct atg gct gaa ggt atc cag gga      3055
322 Thr Thr Pro Met Ser His Ile Val Pro Met Ala Glu Gly Ile Gln Gly
323 870      875      880      885
325 agg caa ctg ggc gct cag tac gag gta cgc gga aca tat gtg gaa agt      3103
326 Arg Gln Ser Gly Ala Gln Tyr Glu Val Arg Gly Thr Tyr Val Glu Ser
327      890      895      900
329 gaa tat gac aat aca aat gac gtg atg cac atg ccc aaa gag tca tat      3151
330 Glu Tyr Asp Asn Thr Asn Asp Val Met His Met Pro Lys Glu Ser Tyr
331      905      910      915
333 tca gtt cag cca gca tcg ttt act tta act acg ggt aac agt tct aac      3199
334 Ser Val Gln Pro Ala Ser Phe Thr Leu Thr Thr Gly Asn Ser Ser Asn
335      920      925      930
337 gaa tat gtt ata aat gat gat cca gta cag att acc att gag aat ccc      3247
338 Glu Tyr Val Ile Asn Asp Asp Pro Val Gln Ile Thr Ile Glu Asn Pro
339      935      940      945
341 gat gat ttt tct aac cct ctt caa cta act gaa gaa tca cac gat atg      3295
342 Asp Asp Phe Ser Asn Pro Leu Gln Leu Thr Glu Glu Ser His Asp Met
343 950      955      960      965

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

DATE: 05/09/2001

PATENT APPLICATION: US/09/430,590E

TIME: 12:13:04

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\05092001\I430590E.raw

L:1161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:1185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:1613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:2131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:2255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:2275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:2323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:2325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:2327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:2365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:2505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:3156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:3184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:3190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:3192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:3278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:3280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:3438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:3502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:3552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:3634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:3654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:3656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:3768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:3770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:3772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:3774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:3776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:3778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:3830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32  
L:3886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:4002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:4004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:5088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/430,590E

DATE: 05/09/2001

TIME: 12:13:04

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\05092001\I430590E.raw

L:6060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:111

L:8916 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139



&lt;210&gt; 150

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

see item 12 on Eon Summary sheet

&lt;400&gt; 150

cgacggctgc agccttcaca ttataattg gc

32

FSE

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.